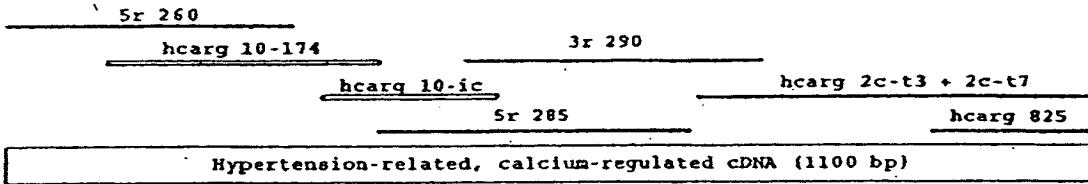


A

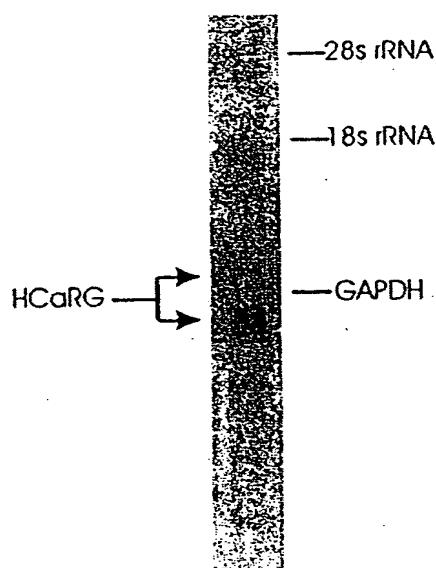


B

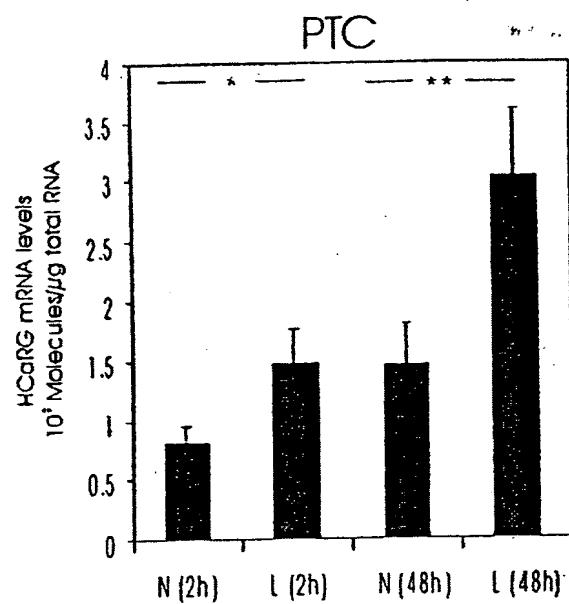
-131	CCACGAGCCACAGCCAGCTACCGCGCTAGGTTCCAGGTGCAGAGGGCG	-80
	ATG TCT GCT TTG GGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC	-1
	Met Ser Ala Leu Gly Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly	60
	CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG ACG GCC GTG GCT CAG CTC TTG	120
	Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln' Leu Leu	
	AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TTG AAA CTT GTA GTC GGG GCC CTG CAT	180
	Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His	
	GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GGT GCC AGC GCC AAC CTG TCA GAA GAG	240
	Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu	
	CGT CTG GCC GTC CTG CTG GCG GCG ACA CAC ACC CTG CTC CAG CAG GCT CTC CGG CTG CCC	300
	Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro	
	CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT CCT CAG	360
	Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Leu Gln Glu Leu Gly Ile Pro Gln	
	GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCT CTT CTC GAC TCT	420
	Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser	
	GTA GCC CAA CAG CAG GGA TCC TCG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC	480
	Val Ala Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp	
	GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CGG AGT GTT CTC ATG CAG CTG	540
	Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val Leu Met Gln Leu	
	AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG	600
	Lys Leu Thr Asp Gly Ser Ala His Arg Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu	
	CGG TAC AGT GTC GCA TTG GTC CTT AAG GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC	660
	Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Glu Lys Lys Cys Glu Arg	
	AAA CTG CAG GAC TGA CTGAACCCTGGTACTGTGGGTGCTGAAGCTGGTACCAAGAACACAGCCCCCACTGGTGA	734
	Lys Leu Gln Asp TER	
	TGACCCCCAACCTCCATTGAGGTCTGCATGTGAGAACGTATTTAAGTGAAGAACAGCGGGACTTCAGGTTTGTTT	813
	ATGAGTCACAGCTGGCAGGGTGGCACAGTTATAATCTCAGCCCTGGAAAGTCTGAGGCTGGAGAATGGGAAGTGT	892
	AGCTGGCCCTGGCTTTCATAGTGAGGCTCAGTGTGAAATTAAAGAGGTAAAGCAACTATTAAAAAAAAAAAAAAA	969

FIGURE 1

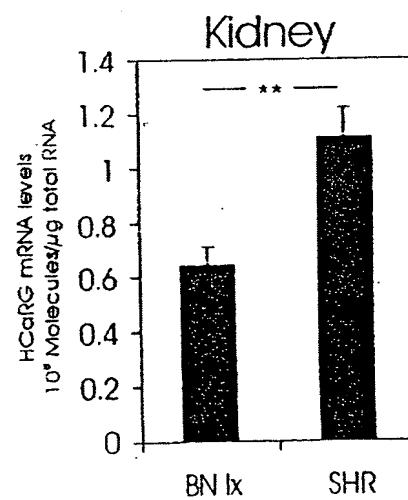
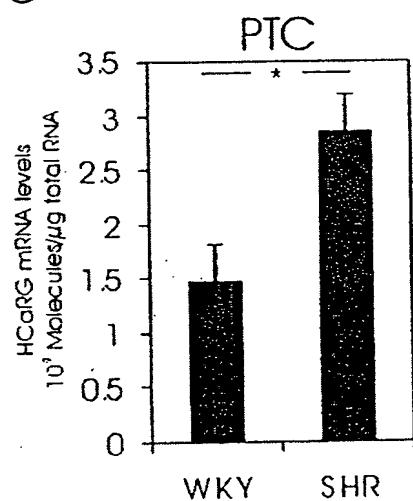
A



B



C



D Kidney

HCaRG →

FIGURE 2

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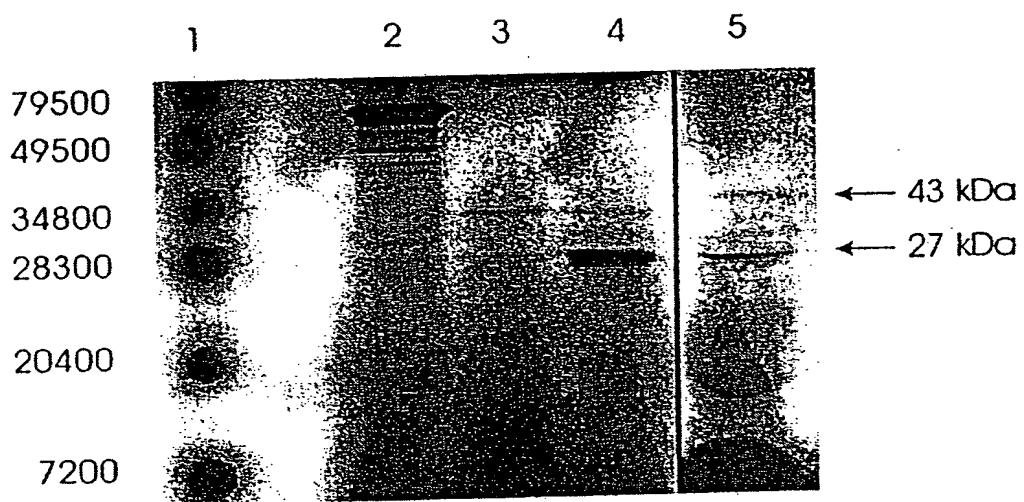


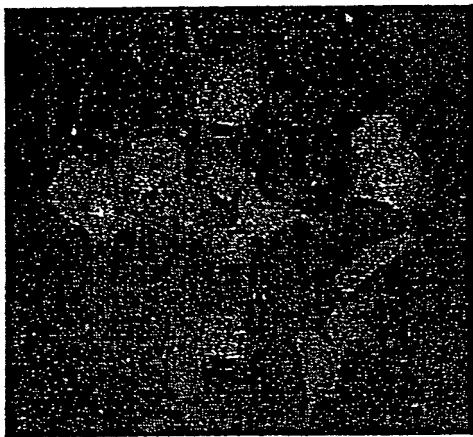
FIGURE 3

Sequence Comparison

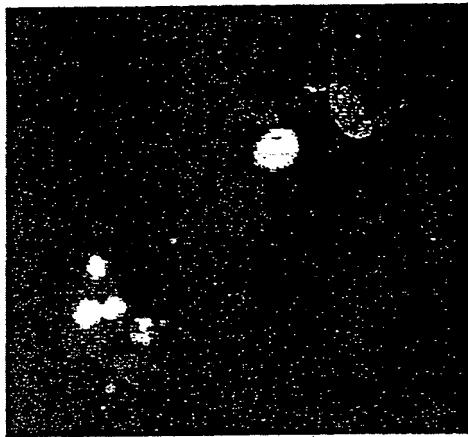
rHCaRG	MSA[APY]EVHPA[QD][G] MSA[VGA]EVHPA[QD][G]	[S]OPS PEVTA[VQ][P] PEVTA[VQ][P]	KIDRSSTERK CDIDRSSTERK	50 50	
rHCaRG	ELK[IVV]GAI[H]GKD[CREA]VEQ LLK[IVV]SSHQ[G]P[CREA]VQR	[L]GASANT[SEE]R[IAV][V][A]GTC LGVSANT[SEE]R[IAV][V][A]GTC	TLT[G][C][R][F] TLE[G][C][R][F]	100 100	
rHCaRG	PASLKPD[E]Q PISLKPD[E]R	E[ELQEL]GIPQ D[CLQEL]CPQ	D[IGDL]ASLA D[NGDL]ASVV	EGSORPLIDS EGSORPLIDS	150 150
rHCaRG	HVS[IFRWRVD]VAISTSAQSR HVA[IFRWRVD]VAISTSALAR	S[LP]PSVLMQL S[LP]PSVLMQL	KI[TDGS]AHRF KI[SDGS]AHRF	EV[E]IAKFOEI EV[E]IAKFOEI	200 200
rHCaRG	RYSVALV[K]KE RYSVALV[K]KE	M[AE]LEK[K]CER M[AE]LEK[K]CER	KLQD KLQD	224 224	

FIGURE 4

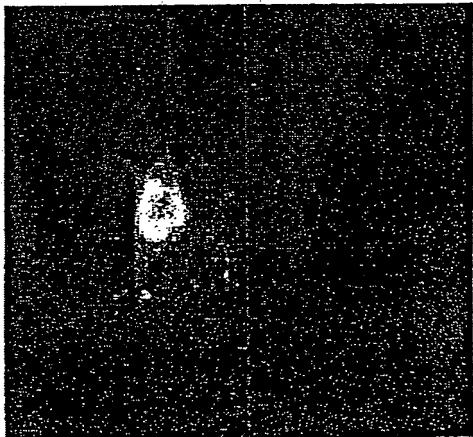
A



B



C



D

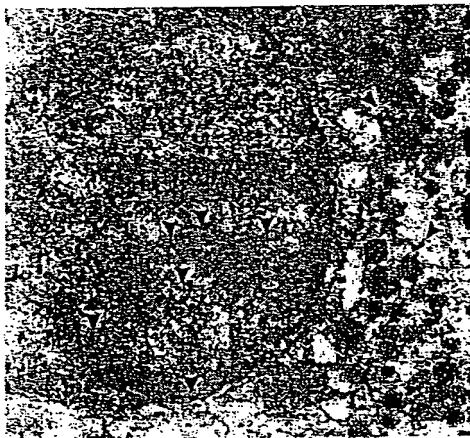
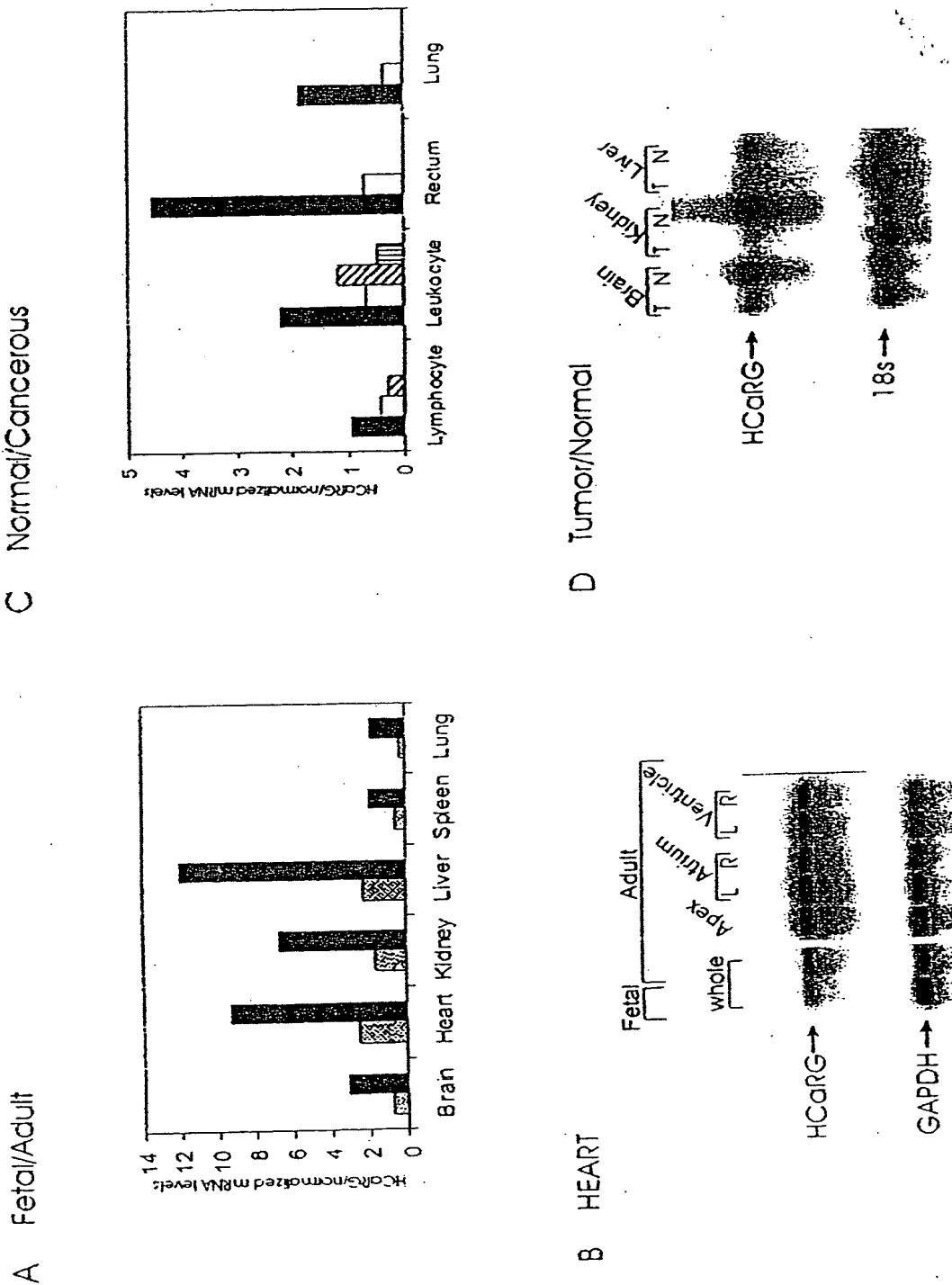


FIGURE 5

FIGURE 6



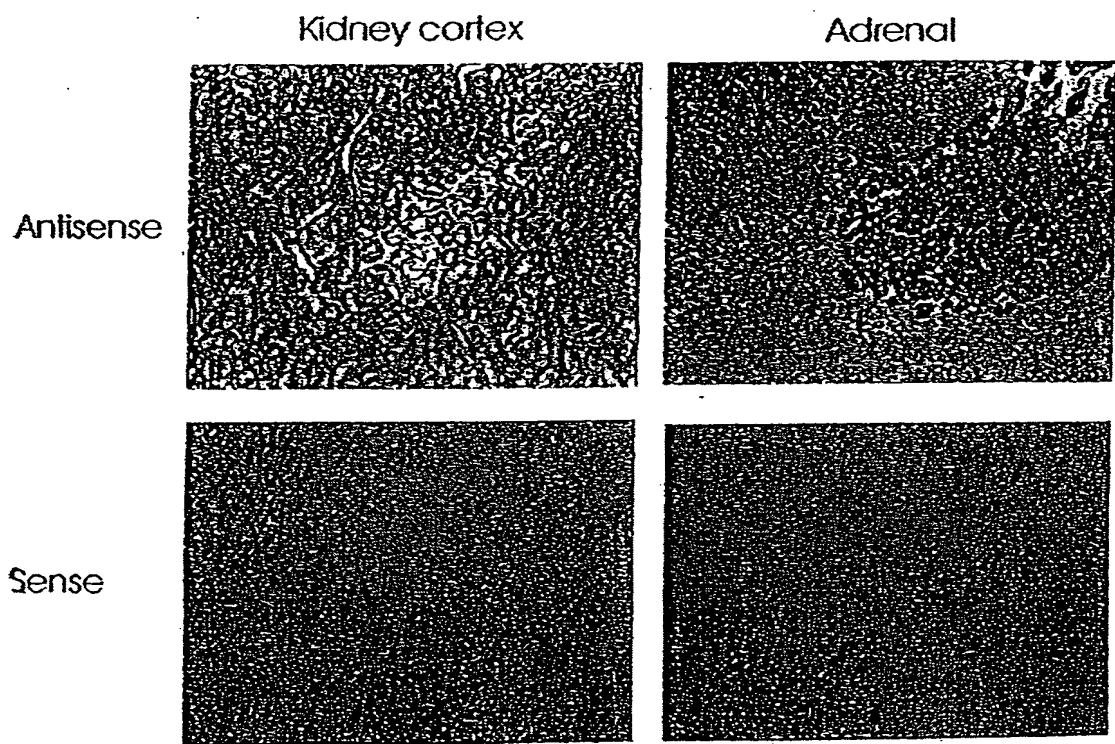
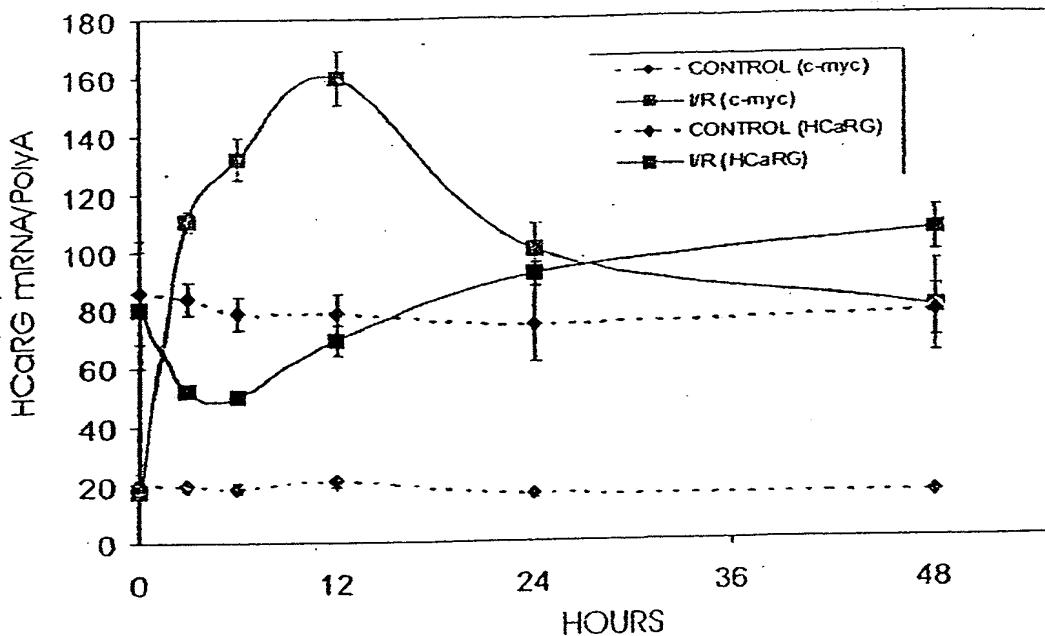
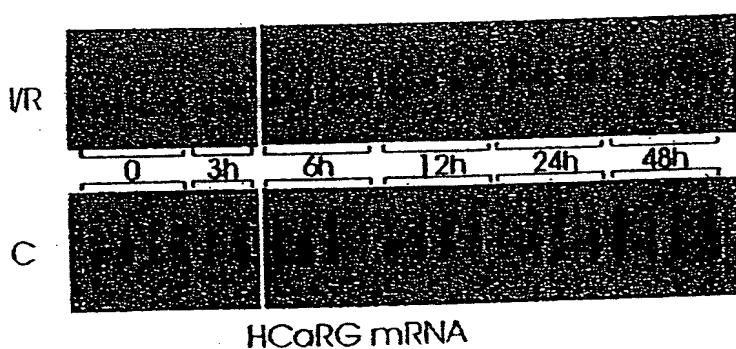


FIGURE 7

A Medulla



B Cortex



C Cortex

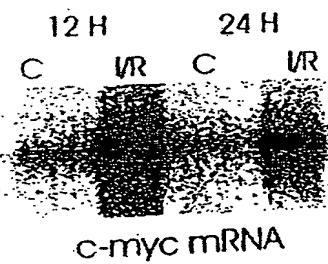
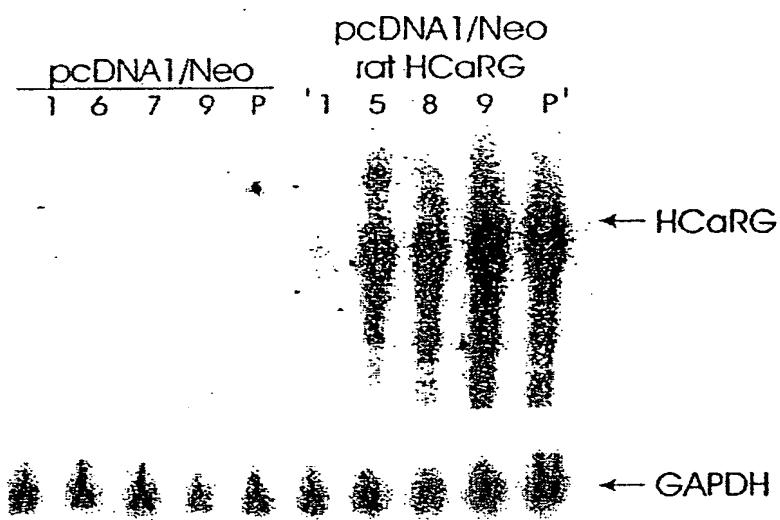


FIGURE 8

A



B

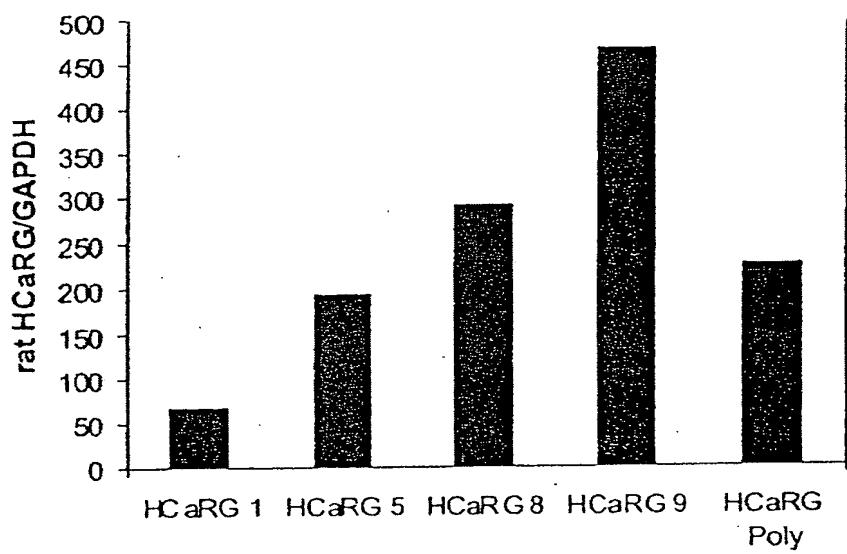
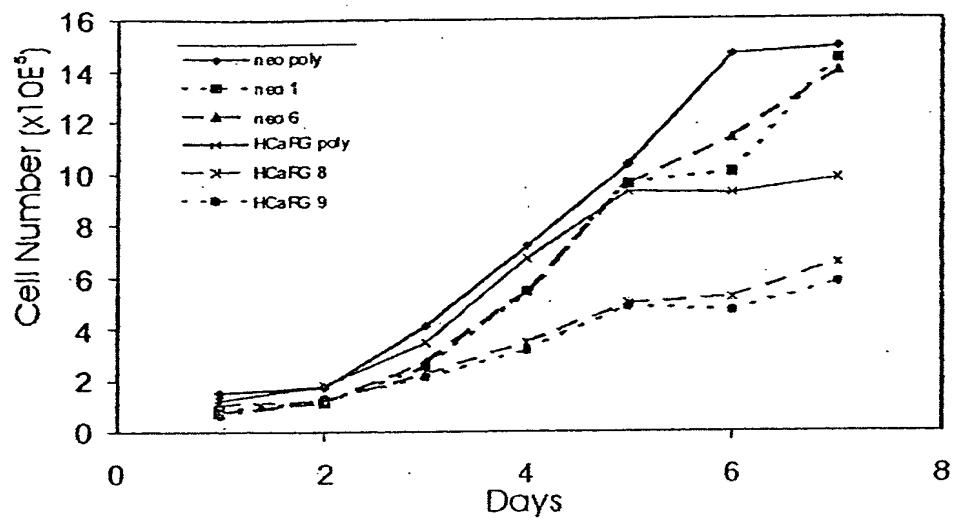


FIGURE 9

A



B

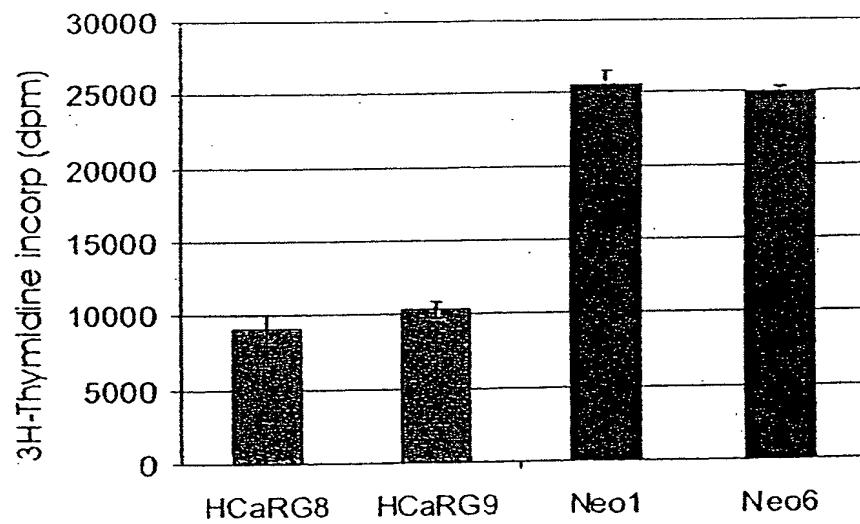


FIGURE 10

FIGURE 11

